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UBPKM <-
function(model,fixed.params,which.quantile=0.95,CV.params=NULL,unif.params=NULL,samples=1000)
{
  sample.vec <- rep(NA,samples)
  for (this.sample in 1:samples)
  {
    these.params <- fixed.params
    for (this.param in names(CV.params))
    {
      these.params[[this.param]] <-
rnorm(1,mean=CV.params[[this.param]]$mean,sd=CV.params[[this.param]]$mean*CV.params[[this.param]]$CV)
    }
    for (this.param in names(unif.params))
    {
      these.params[[this.param]] <-
runif(1,min=unif.params[[this.param]]$min,max=unif.params[[this.param]]$max)
    }
    sample.vec[this.sample] <- call(model,these.params)
  }

  return(quantile(sample.vec,which.quantile))
}

Calc_1comp_Css <- function(chem.name=NULL,chem.CAS=NULL,daily.dose=1,which.quantile=0.95)
{
}

Wetmore_Css(chem.CAS="94-82-6")
Wetmore_Css(chem.CAS="94-82-6",which.quantile=0.5)

calc_Css(chem.CAS="94-82-6")

Wetmore_Oral_Equiv(4,chem.CAS="94-82-6")
Wetmore_Oral_Equiv(6,chem.CAS="94-82-6")
Wetmore_Oral_Equiv(6,chem.CAS="94-82-6",species="Rat")
Wetmore_Oral_Equiv(6,chem.CAS="94-75-7",species="Rat",which.quantile=0.5)

Wetmore.human.values <- NULL
vLiver.human.values <- NULL
for (this.CAS in Wetmore.Human.CASlist)
  if (this.CAS %in% vLiver.Human.CASlist)
  {
    Wetmore.human.values[this.CAS] <- Wetmore_Css(chem.CAS=this.CAS,which.quantile=0.5)
    vLiver.human.values[this.CAS] <- calc_Css(chem.CAS=this.CAS)
  }

plot(vLiver.human.values,Wetmore.human.values,log="xy")
matplot(c(10^-3,10^2),c(10^-3,10^2),lty=2,add=T,type="l")

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